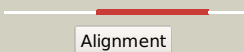

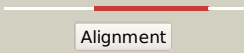

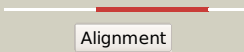

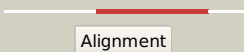

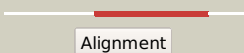

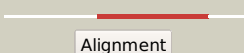

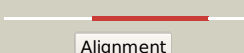




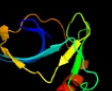
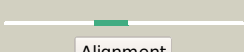

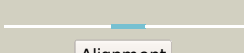
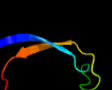
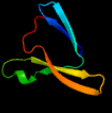







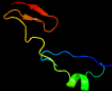


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2405 (-) _2703279_2703848
Date	Wed Aug 7 12:50:02 BST 2019
Unique Job ID	aa0ca4c1335f8972

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4mzpC_	 Alignment		99.8	15	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
2	d1ne8a_	 Alignment		99.8	20	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
3	c5hjaz_	 Alignment		99.7	18	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
4	d1m1fa_	 Alignment		99.7	19	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
5	d1ub4a_	 Alignment		99.5	16	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
6	c5hk3B_	 Alignment		99.5	22	PDB header: hydrolase/dna Chain: B: PDB Molecule: endoribonuclease mazf6; PDBTitle: crystal structure of m. tuberculosis mazf-mt3 t52d-f62d mutant in2 complex with dna
7	c5wygC_	 Alignment		99.5	15	PDB header: hydrolase Chain: C: PDB Molecule: probable endoribonuclease mazf7; PDBTitle: the crystal structure of the apo form of mtb mazf
8	c5xe3B_	 Alignment		99.3	13	PDB header: hydrolase/antitoxin Chain: B: PDB Molecule: endoribonuclease mazf4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
9	c5ccaA_	 Alignment		99.1	19	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease mazf3; PDBTitle: crystal structure of mtb toxin
10	c2x35A_	 Alignment		45.7	33	PDB header: transcription Chain: A: PDB Molecule: peregrin; PDBTitle: molecular basis of histone h3k36me3 recognition by the pwp domain of2 brpf1.
11	c5ikjA_	 Alignment		30.3	33	PDB header: transcription Chain: A: PDB Molecule: cryptic loci regulator 2; PDBTitle: structure of clr2 bound to the clr1 c-terminus

12	d1sg5a1	Alignment		29.6	12	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: Rof-like
13	c3lyiA	Alignment		27.1	43	PDB header: transcription Chain: A; PDB Molecule: bromodomain-containing protein 1; PDBTitle: pwwp domain of human bromodomain-containing protein 1
14	c3rlhA	Alignment		26.1	25	PDB header: hydrolase Chain: A; PDB Molecule: sphingomyelin phosphodiesterase d lisictox-alpha1a; PDBTitle: crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
15	c3pfsA	Alignment		22.3	40	PDB header: protein binding Chain: A; PDB Molecule: bromodomain and phd finger-containing protein 3; PDBTitle: pwwp domain of human bromodomain and phd finger-containing protein 3
16	d1h3za	Alignment		19.8	57	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
17	c5uoiA	Alignment		19.2	31	PDB header: de novo protein Chain: A; PDB Molecule: hhh_rd1_0142; PDBTitle: solution structure of the de novo mini protein hhh_rd1_0142
18	c2gfuA	Alignment		18.7	29	PDB header: dna binding protein Chain: A; PDB Molecule: dna mismatch repair protein msh6; PDBTitle: nmr solution structure of the pwwp domain of mismatch2 repair protein hmsh6
19	d2nlua1	Alignment		16.8	29	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
20	c2hz6A	Alignment		16.7	28	PDB header: signaling protein Chain: A; PDB Molecule: endoplasmic reticulum to nucleus signalling 1 PDBTitle: the crystal structure of human ire1-alpha luminal domain
21	c3id6A	Alignment	not modelled	15.3	22	PDB header: transferase Chain: A; PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus nop5 (1-262) and2 fibrillar in complex
22	c6g25A	Alignment	not modelled	12.9	43	PDB header: oncoprotein Chain: A; PDB Molecule: histone-lysine n-methyltransferase nsd3; PDBTitle: x-ray structure of nsd3-pwwp1 in complex with compound 4
23	c2z6vA	Alignment	not modelled	12.9	23	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf9 from2 mycobacterium avium
24	c2l89A	Alignment	not modelled	12.8	18	PDB header: protein binding Chain: A; PDB Molecule: pwwp domain-containing protein 1; PDBTitle: solution structure of pdp1 pwwp domain reveals its unique binding2 sites for methylated h4k20 and dna
25	c2jvwA	Alignment	not modelled	12.7	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117
26	d1n27a	Alignment	not modelled	12.3	19	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
27	c6nd4a	Alignment	not modelled	11.2	22	PDB header: ribosome Chain: A; PDB Molecule: mpp10; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
28	c3rlgA	Alignment	not modelled	9.6	25	PDB header: hydrolase Chain: A; PDB Molecule: sphingomyelin phosphodiesterase d lisictox-alpha1a; PDBTitle: crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant

29	d2daq1	Alignment	not modelled	9.5	50	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
30	c2fwtA	Alignment	not modelled	9.5	20	PDB header: electron transport Chain: A: PDB Molecule: dhc, diheme cytochrome c; PDBTitle: crystal structure of dhc purified from rhodobacter2 sphaeroides
31	d1e5ra	Alignment	not modelled	8.0	17	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase)
32	c2nnwC	Alignment	not modelled	7.6	33	PDB header: transferase Chain: C: PDB Molecule: nop5/nop56 related protein; PDBTitle: alternative conformations of nop56/58-fibrillarin complex and2 implication for induced-fit assenly of box c/d rnps
33	c5gz5A	Alignment	not modelled	7.2	20	PDB header: hydrolase Chain: A: PDB Molecule: snake venom phosphodiesterase (pde); PDBTitle: crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra) in complex with amp
34	c4fu6A	Alignment	not modelled	7.0	18	PDB header: transcription Chain: A: PDB Molecule: pc4 and sfrs1-interacting protein; PDBTitle: crystal structure of the psp1 pwwp domain
35	c2zq5A	Alignment	not modelled	6.7	29	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)
36	c3bxpA	Alignment	not modelled	6.5	10	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcfs1 at 1.70 a resolution
37	d1tafb	Alignment	not modelled	6.5	21	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
38	c3u99A	Alignment	not modelled	6.3	15	PDB header: electron transport Chain: A: PDB Molecule: diheme cytochrome c; PDBTitle: the experimental x-ray structure of the new diheme cytochrome type c2 from shewanella baltica os155 sb-dhc
39	d1aopa1	Alignment	not modelled	6.0	8	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
40	c6nd4b	Alignment	not modelled	6.0	22	PDB header: ribosome Chain: B: PDB Molecule: PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
41	c5volA	Alignment	not modelled	5.6	18	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: bacint_04212 ferulic acid esterase
42	d2exda1	Alignment	not modelled	5.5	22	Fold: OB-fold Superfamily: NfeD domain-like Family: NfeD domain-like
43	c3ggzH	Alignment	not modelled	5.3	39	PDB header: protein transport, endocytosis Chain: H: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
44	c1mtpB	Alignment	not modelled	5.2	32	PDB header: structural genomics Chain: B: PDB Molecule: serine proteinase inhibitor (serpin), chain b; PDBTitle: the x-ray crystal structure of a serpin from a thermophilic prokaryote
45	c3id5E	Alignment	not modelled	5.0	22	PDB header: transferase/ribosomal protein/rna Chain: E: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarin, l7ae and a split half c/d rna
46	c4nm5B	Alignment	not modelled	5.0	50	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of gsk-3/axin complex bound to phosphorylated wnt2 receptor lrp6 c-motif
47	c4nm3B	Alignment	not modelled	5.0	50	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of gsk-3/axin complex bound to phosphorylated n-2 terminal auto-inhibitory ps9 peptide
48	c4nu1B	Alignment	not modelled	5.0	50	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of a transition state mimic of the gsk-3/axin2 complex bound to phosphorylated n-terminal auto-inhibitory ps93 peptide